

## SEQUENCE LISTING

<110> Burkly, Linda C.

<120> TREATMENT FOR INSULIN DEPENDENT DIABETES

<130> 10274-008003

<140> US 09/234,290

<141> 1999-01-20

<150> US 08/447,118

<151> 1993-05-22

<150> US 08/029,330

<151> 1993-02-09

<150> PCT/US94/01456

<151> 1994-02-09

<160> 19

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 360

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (0)...(0)

<223> pBAG159 insert: HP1/2 heavy  
chain variableregion; amino acid 1  
is Glu (E) but Gln (Q) may be substituted

<221> CDS

<222> (1)...(360)

<400> 1

gtc	aaa	ctg	cag	cag	tct	ggg	gca	gag	ctt	gtg	aag	cca	ggg	gcc	tca	48
Val	Lys	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Lys	Pro	Gly	Ala	Ser	
1				5					10					15		

gtc	aag	ttg	tcc	tgc	aca	gct	tct	ggc	ttc	aac	att	aaa	gac	acc	tat	96
Val	Lys	Leu	Ser	Cys	Thr	Ala	Ser	Gly	Phe	Asn	Ile	Lys	Asp	Thr	Tyr	
			20						25					30		

atg	cac	tgg	gtg	aag	cag	agg	cct	gaa	cag	ggc	ctg	gag	tgg	att	gga	144
Met	His	Trp	Val	Lys	Gln	Arg	Pro	Glu	Gln	Gly	Leu	Glu	Trp	Ile	Gly	
			35				40					45				

agg	att	gat	cct	gcg	agt	ggc	gat	act	aaa	tat	gac	ccg	aag	ttc	cag	192
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JUN 16 2000

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Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
 50                      55                      60

gtc aag gcc act att aca gcg gac acg tcc tcc aac aca gcc tgg ctg      240
Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
 65                      70                      75                      80

cag ctc agc agc ctg aca tct gag gac act gcc gtc tac tac tgt gca      288
Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                      85                      90                      95

gac gga atg tgg gta tca acg gga tat gct ctg gac ttc tgg ggc caa      336
Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
                      100                      105                      110

ggg acc acg gtc acc gtc tcc tca      360
Gly Thr Thr Val Thr Val Ser Ser
                      115                      120

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<210> 2
<211> 120
<212> PRT
<213> Homo sapiens

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Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
                35                      40                      45
Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
                50                      55                      60
Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
                65                      70                      75                      80
Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                      90                      95
Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
                100                      105                      110
Gly Thr Thr Val Thr Val Ser Ser
                115                      120

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<210> 3
<211> 318
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (0)...(0)
<223> pBAG172 insert: HP1/2
      light chain variable region

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<221> CDS
<222> (1)...(318)

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<223> HP1/2 light chain variable region

<400> 3

agt att gtg atg acc cag act ccc aaa ttc ctg ctt gtt tca gca gga	48
Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly	
1 5 10 15	
gac agg gtt acc ata acc tgc aag gcc agt cag agt gtg act aat gat	96
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp	
20 25 30	
gta gct tgg tac caa cag aag cca ggg cag tct cct aaa ctg ctg ata	144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile	
35 40 45	
tat tat gca tcc aat cgc tac act gga gtc cct gat cgc ttc act ggc	192
Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly	
50 55 60	
agt gga tat ggg acg gat ttc act ttc acc atc agc act gtg cag gct	240
Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala	
65 70 75 80	
gaa gac ctg gca gtt tat ttc tgt cag cag gat tat agc tct ccg tac	288
Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr	
85 90 95	
acg ttc gga ggg ggg acc aag ctg gag atc	318
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile	
100 105	

<210> 4

<211> 106

<212> PRT

<213> Homo sapiens

<400> 4

Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly	
1 5 10 15	
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp	
20 25 30	
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile	
35 40 45	
Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly	
50 55 60	
Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala	
65 70 75 80	
Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr	
85 90 95	
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile	
100 105	

<210> 5

<211> 429

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(429)

<221> sig\_peptide

<222> (1)...(57)

<221> mat\_peptide

<222> (58)...(429)

<221> misc\_feature

<222> (0)...(0)

<223> pBAG195 insert: AS heavy chain variable region

<400> 5

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Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly	
-15 -10 -5	

gcc cac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga	96
Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg	
1 5 10	

cct agc cag acc ctg agc ctg acc tgc acc gcg tct ggc ttc aac att	144
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile	
15 20 25	

aaa gac acc tat atg cac tgg gtg aga cag cca cct gga cga ggt ctt	192
Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu	
30 35 40 45	

gag tgg att gga agg att gat cct gcg agt ggc gat act aaa tat gac	240
Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp	
50 55 60	

ccg aag ttc cag gtc aga gtg aca atg ctg gta gac acc agc agc aac	288
Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Ser Asn	
65 70 75	

cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtc	336
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val	
80 85 90	

tat tat tgt gca gac gga atg tgg gta tca acg gga tat gct ctg gac	384
Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp	
95 100 105	

ttc tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt gag tcc	429
Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser	
110 115 120	

<210> 6

<211> 143

<212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> (1)...(19)

<400> 6  
 Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly  
                   -15                  -10                  -5  
 Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg  
                   1                  5                  10  
 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile  
           15                  20                  25  
 Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu  
 30                  35                  40                  45  
 Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp  
                   50                  55                  60  
 Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Ser Asn  
                   65                  70                  75  
 Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
           80                  85                  90  
 Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp  
           95                  100                  105  
 Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser  
 110                  115                  120

<210> 7  
 <211> 384  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(384)

<221> sig\_peptide  
 <222> (1)...(57)

<221> mat\_peptide  
 <222> (58)...(384)

<221> misc\_feature  
 <222> (0)...(0)  
 <223> pBAG198 insert: VK (SVMDY) light chain variable  
           region

<400> 7  
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 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
                   -15                  -10                  -5  
 gtc cac tcc agc atc gtg atg acc cag agc cca agc agc ctg agc gcc 96  
 Val His Ser Ser Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
           1                  5                  10

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agc gtg ggt gac aga gtg acc atc acc tgt aag gcc agt cag agt gtg      144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val
    15                20                25

act aat gat gta gct tgg tac cag cag aag cca ggt aag gct cca aag      192
Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
    30                35                40                45

ctg ctg atc tac tat gca tcc aat cgc tac act ggt gtg cca gat aga      240
Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg
                50                55                60

ttc agc ggt agc ggt tat ggt acc gac ttc acc ttc acc atc agc agc      288
Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
                65                70                75

ctc cag cca gag gac atc gcc acc tac tac tgc cag cag gat tat agc      336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser
                80                85                90

tct ccg tac acg ttc ggc caa ggg acc aag gtg gaa atc aaa cgt aag      384
Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys
    95                100                105

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<210> 8  
 <211> 128  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> (1)...(19)

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<400> 8
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
          -15                -10                -5
Val His Ser Ser Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
          1                5                10
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val
    15                20                25
Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
    30                35                40                45
Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg
                50                55                60
Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
                65                70                75
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser
    80                85                90
Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys
    95                100                105

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<210> 9  
 <211> 1347  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(1338)

<221> misc\_feature  
 <222> (1)...(219)  
 <223> VCAM-1 gene segment: This portion of the sequence corresponds, in part, to Exons I, II and III nucleotide sequence of Cybulsky et al. Proc. Nat'l. Acad. Sci. USA 88: 7861 (1991).

<221> misc\_feature  
 <222> (220)...(229)  
 <223> Hinge region: This portion of the sequence corresponds, in part, to Exons I, II and III nucleotide sequence of Cybulsky et al. Proc. Nat'l. Acad. Sci. USA 88: 7861 (1991).

<221> misc\_feature  
 <222> (230)...(338)  
 <223> Heavy chain constant region 2: This portion of the sequence corresponds, in part, to Fig. 12A in PCT/US92/02050 and represents the heavy chain constant region 2 of Human IgG1 heavy chain constant region.

<221> misc\_feature  
 <222> (339)...(446)  
 <223> Heavy chain constant region 3: This portion of the sequence corresponds, in part, to Fig. 12A in PCT/US92/02050 and represents the heavy chain constant region 3 of Human IgG1 heavy chain constant region.

<400> 9  
 atg cct ggg aag atg gtc gtg atc ctt gga gcc tca aat ata ctt tgg 48  
 Met Pro Gly Lys Met Val Val Ile Leu Gly Ala Ser Asn Ile Leu Trp  
 1 5 10 15  
 ata atg ttt gca gct tct caa gct ttt aaa atc gag acc acc cca gaa 96  
 Ile Met Phe Ala Ala Ser Gln Ala Phe Lys Ile Glu Thr Thr Pro Glu  
 20 25 30  
 tct aga tat ctt gct cag att ggt gac tcc gtc tca ttg act tgc agc 144  
 Ser Arg Tyr Leu Ala Gln Ile Gly Asp Ser Val Ser Leu Thr Cys Ser  
 35 40 45  
 acc aca ggc tgt gag tcc cca ttt ttc tct tgg aga acc cag ata gat 192  
 Thr Thr Gly Cys Glu Ser Pro Phe Phe Ser Trp Arg Thr Gln Ile Asp  
 50 55 60  
 agt cca ctg aat ggg aag gtg acg aat gag ggg acc aca tct acg ctg 240  
 Ser Pro Leu Asn Gly Lys Val Thr Asn Glu Gly Thr Thr Ser Thr Leu

65	70	75	80	
aca atg aat cct gtt agt ttt ggg aac gaa cac tct tac ctg tgc aca				288
Thr Met Asn Pro Val Ser Phe Gly Asn Glu His Ser Tyr Leu Cys Thr	85	90	95	
gca act tgt gaa tct agg aaa ttg gaa aaa gga atc cag gtg gag atc				336
Ala Thr Cys Glu Ser Arg Lys Leu Glu Lys Gly Ile Gln Val Glu Ile	100	105	110	
tac tct ttt cct aag gat cca gag att cat ttg agt ggc cct ctg gag				384
Tyr Ser Phe Pro Lys Asp Pro Glu Ile His Leu Ser Gly Pro Leu Glu	115	120	125	
gct ggg aag ccg atc aca gtc aag tgt tca gtt gct gat gta tac cca				432
Ala Gly Lys Pro Ile Thr Val Lys Cys Ser Val Ala Asp Val Tyr Pro	130	135	140	
ttt gac agg ctg gag ata gac tta ctg aaa gga gat cat ctc atg aag				480
Phe Asp Arg Leu Glu Ile Asp Leu Leu Lys Gly Asp His Leu Met Lys	145	150	155	160
agt cag gaa ttt ctg gag gat gca gac agg aag tcc ctg gaa acc aag				528
Ser Gln Glu Phe Leu Glu Asp Ala Asp Arg Lys Ser Leu Glu Thr Lys	165	170	175	
agt ttg gaa gta acc ttt act cct gtc att gag gat att gga aaa gtt				576
Ser Leu Glu Val Thr Phe Thr Pro Val Ile Glu Asp Ile Gly Lys Val	180	185	190	
ctt gtt tgc cga gct aaa tta cac att gat gaa atg gat tct gtg ccc				624
Leu Val Cys Arg Ala Lys Leu His Ile Asp Glu Met Asp Ser Val Pro	195	200	205	
aca gta agg cag gct gta aaa gaa ttg caa gtc gac aaa act cac aca				672
Thr Val Arg Gln Ala Val Lys Glu Leu Gln Val Asp Lys Thr His Thr	210	215	220	
tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc				720
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe	225	230	235	240
ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct				768
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro	245	250	255	
gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc				816
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val	260	265	270	
aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca				864
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr	275	280	285	
aag ccg cgg gag gag cag tac aac agc acg tac cgg gtg gtc agc gtc				912
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val	290	295	300	



ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc 960  
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys  
 305 310 315 320

aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc 1008  
 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser  
 325 330 335

aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca 1056  
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro  
 340 345 350

tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc 1104  
 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val  
 355 360 365

aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg 1152  
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly  
 370 375 380

cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac 1200  
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp  
 385 390 395 400

ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg 1248  
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp  
 405 410 415

cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac 1296  
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His  
 420 425 430

aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa 1338  
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 435 440 445

tgagtgcgg 1347

<210> 10  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide for PCR

<400> 10  
 tcgtcgacaa aactcacaca tgcc

24

<210> 11  
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 <212> DNA  
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<220>  
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<400> 11  
 gtaaagtagt gcggcgccgc ccaa 24

<210> 12  
 <211> 115  
 <212> DNA  
 <213> Artificial Sequence

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 tgctcgagct ctatgatctg attccatgga tctcacatc ccaatccgcg gccgc 115

<210> 13  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide for PCR

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<210> 14  
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 <213> Artificial Sequence

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 aagtcgactt gcaattcttt tac 23

<210> 15  
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 tcgacgcggc cgcg 14

<210> 16  
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 <212> PRT  
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<400> 16  
 Met Pro Gly Lys Met Val Val Ile Leu Gly Ala Ser Asn Ile Leu Trp  
 1 5 10 15

Ile	Met	Phe	Ala 20	Ala	Ser	Gln	Ala 25	Phe	Lys	Ile	Glu	Thr	Thr 30	Pro	Glu
Ser	Arg	Tyr 35	Leu	Ala	Gln	Ile	Gly 40	Asp	Ser	Val	Ser	Leu 45	Thr	Cys	Ser
Thr	Thr 50	Gly	Cys	Glu	Ser	Pro 55	Phe	Phe	Ser	Trp	Arg 60	Thr	Gln	Ile	Asp
Ser 65	Pro	Leu	Asn	Gly	Lys 70	Val	Thr	Asn	Glu	Gly 75	Thr	Thr	Ser	Thr	Leu 80
Thr	Met	Asn	Pro	Val 85	Ser	Phe	Gly	Asn	Glu 90	His	Ser	Tyr	Leu	Cys 95	Thr
Ala	Thr	Cys	Glu 100	Ser	Arg	Lys	Leu	Glu 105	Lys	Gly	Ile	Gln	Val 110	Glu	Ile
Tyr	Ser	Phe 115	Pro	Lys	Asp	Pro	Glu 120	Ile	His	Leu	Ser	Gly 125	Pro	Leu	Glu
Ala	Gly 130	Lys	Pro	Ile	Thr	Val 135	Lys	Cys	Ser	Val	Ala 140	Asp	Val	Tyr	Pro
Phe 145	Asp	Arg	Leu	Glu	Ile 150	Asp	Leu	Leu	Lys	Gly 155	Asp	His	Leu	Met	Lys 160
Ser	Gln	Glu	Phe 165	Leu	Glu	Asp	Ala	Asp	Arg 170	Lys	Ser	Leu	Glu	Thr 175	Lys
Ser	Leu	Glu	Val 180	Thr	Phe	Thr	Pro	Val 185	Ile	Glu	Asp	Ile	Gly 190	Lys	Val
Leu	Val	Cys 195	Arg	Ala	Lys	Leu	His 200	Ile	Asp	Glu	Met	Asp 205	Ser	Val	Pro
Thr	Val 210	Arg	Gln	Ala	Val	Lys 215	Glu	Leu	Gln	Val	Asp 220	Lys	Thr	His	Thr
Cys 225	Pro	Pro	Cys	Pro	Ala 230	Pro	Glu	Leu	Leu	Gly 235	Pro	Ser	Val	Phe	240
Leu	Phe	Pro	Pro	Lys 245	Pro	Lys	Asp	Thr	Leu 250	Met	Ile	Ser	Arg	Thr 255	Pro
Glu	Val	Thr	Cys 260	Val	Val	Val	Asp 265	Val	Ser	His	Glu	Asp	Pro 270	Glu	Val
Lys	Phe 275	Asn	Trp	Tyr	Val	Asp 280	Gly	Val	Glu	Val	His 285	Asn	Ala	Lys	Thr
Lys	Pro 290	Arg	Glu	Glu	Gln	Tyr 295	Asn	Ser	Thr	Tyr	Arg 300	Val	Val	Ser	Val
Leu 305	Thr	Val	Leu	His	Gln 310	Asp	Trp	Leu	Asn	Gly 315	Lys	Glu	Tyr	Lys	Cys 320
Lys	Val	Ser	Asn 325	Lys	Ala	Leu	Pro	Ala	Pro 330	Ile	Glu	Lys	Thr	Ile	Ser
Lys	Ala	Lys	Gly 340	Gln	Pro	Arg	Glu	Pro 345	Gln	Val	Tyr	Thr	Leu 350	Pro	Pro
Ser	Arg	Asp 355	Glu	Leu	Thr	Lys	Asn 360	Gln	Val	Ser	Leu	Thr 365	Cys	Leu	Val
Lys	Gly 370	Phe	Tyr	Pro	Ser	Asp 375	Ile	Ala	Val	Glu	Trp 380	Glu	Ser	Asn	Gly
Gln 385	Pro	Glu	Asn	Asn	Tyr 390	Lys	Thr	Thr	Pro	Pro 395	Val	Leu	Asp	Ser	Asp 400
Gly	Ser	Phe	Phe 405	Leu	Tyr	Ser	Lys	Leu	Thr 410	Val	Asp	Lys	Ser	Arg	Trp
Gln	Gln	Gly	Asn 420	Val	Phe	Ser	Cys	Ser 425	Val	Met	His	Glu	Ala 430	Leu	His
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<210> 17

<211> 6

<212> PRT  
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<220>  
<223> synthetically generated peptide

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1 5

<210> 18  
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<212> PRT  
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<220>  
<223> synthetically generated peptide

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<210> 19  
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<212> PRT  
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1 5